1

SEQUENCE LISTING

<110> GlycoDesign Inc. <120> Novel N-Acetylglycosaminyltransferase Genes <130> p174pct5 <140> <141> <150> U.S. 60/095,919 <151> 1998-08-07 <160> 16 <170> PatentIn Ver. 2.0 <210> 1 <211> 2061 <212> DNA <213> Homo sapiens <400> 1 atgtttttta caatctcaag aaaaaatatg tcccagaaat tgagtttact gttgcttgta 60 tttggactca tttggggatt gatgttactg cactatactt ttcaacaacc aagacatcaa 120 agcagtgtca agttacgtga gcaaatacta gacttaagca aaagatatgt taaagctcta 180

gcagaggaaa ataagaacac agtggatgtc gagaacggtg cttctatggc aggatatgcg 240

gatetgaaaa gaacaattge tgtccttctg gatgacattt tgcaacgatt ggtgaagctg 300

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Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu Arg Glu Gln

35 40 45

Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu Ala Glu Glu Asn

50 55 60

Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser Met Ala Gly Tyr Ala

 65
 70
 75
 80

Asp Leu Lys Arg Thr Ile Ala Val Leu Leu Asp Asp Ile Leu Gln Arg

90 95

Leu Val Lys Leu Glu Asn Lys Val Asp Tyr Ile Val Val Asn Gly Ser

100 105 110

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4,

PCT/CA99/00711

Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr	Ser	Gly	Asn	Leu	Val	Pro	Val	Thr
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Thr Asn Lys Arg Thr Asn Val Ser Gly Ser Ile Arg Ile Ala Val Glu
130 135 140

Asn His Leu Val Leu Leu His Pro Leu Trp Ile Ile Ser Tyr Gly Arg

Lys Ala Leu Tyr Cys Trp Leu Arg Thr Glu Ala Ile Leu Tyr Asn Lys

165 170 175

Ser Thr Asn Gly Gly Gln Asp Lys Cys Val Phe Pro Pro Ile Asp Gly
180 185 190

Tyr Pro His Tyr Glu Gly Lys Ile Lys Trp Ile Asn Asp Met Cys Arg
195 200 205

Ser Asp Pro Cys Lys Ala His Tyr Gly Ile Asp Gly Ser Ser Cys Thr 210 215 220

Phe Phe Ile Tyr Leu Ser Asp Ala Asp Asn His Cys Pro His Ala Pro
225 230 235 240

Trp Arg His Lys Asn Pro Tyr Asp Asp Ala Glu His Asn Ser Cys Ala

245 250 255

Glu Ile Arg Ser Asp Phe Glu Leu Leu Tyr Ser Val Ile His His Lys
260 265 270

Asp	Glu	Phe	His	Phe	Met	Arg	Leu	Arg	Arg	Arg	Arg	Met	Val	Glu	Gly
		275					280					285			

Trp Ala Gln Ile Ala Lys Ser Leu Ala Asp Lys Gln Asn Ala Glu Lys
290 295 300

Lys Lys Arg Lys Lys Ala Leu Val His Leu Gly Ile Ile Thr Lys Asp
305 310 315 320

Thr Val Ser Lys Ile Ala Glu Thr Gly Phe Ser Ala Ala Pro Leu Gly
325 330 335

Asp Leu Val His Trp Ser Asp Val Ile Thr Ser Ala Tyr Ala Ala Gly
340 345 350

His Asp Val Arg Ile Thr Ala Ser Leu Ala Glu Leu Lys Asp Val Val
355 360 365

Lys Lys Ile Ile Gly Asn Arg Ser Gly Cys Pro Ser Val Gly Asp Arg 370 375 380

Ile Val Glu Leu Leu Tyr Ala Asp Val Ile Gly Leu Gly Gln Phe Lys
385 390 395 400

Lys Thr Leu Gly Pro Thr Trp Ala Gln His Arg Trp Met Val Arg Val
405 410 415

Leu Glu Thr Phe Gly Ser Asp Pro Asp Phe Glu His Ala Asn Tyr Ala

6

420 425 430

Gln Thr Lys Gly His Lys Ser Pro Trp Gly Trp Trp Asn Leu Asn Pro
435 440 445

Asn Asn Phe Tyr Thr Met Phe Pro His Thr Pro Glu Asn Thr Phe Leu
450 455 460

Gly Phe Ala Ile Glu Gln His Leu Asn Ser Ser Asp Met His His Leu
465 470 475 480

Asn Glu Met Lys Arg Gln Asn Gln Thr Leu Val Tyr Gly Lys Val Asp
485
490
495

Ser Phe Trp Lys Asn Lys His Ile Tyr Phe Glu Ile Ile His Asn Tyr
500 505 510

Ile Glu Val Gln Ala Thr Val Tyr Asp Ser Ser Thr Pro Asn Ile Pro
515 520 525

Ser Tyr Ser Arg Asn His Gly Ile Leu Ser Gly Arg Asp His Arg Phe
530 535 540

Leu Leu Arg Glu Thr Phe Leu Leu Gly Leu Gly Thr Pro Tyr Glu
545 550 555 560

Arg Cys Ala Pro Leu Glu Ala Met Ala Asn Arg Cys Val Phe Leu Lys
565 570 575

7.

Pro Lys Phe Pro Pro Pro Asn Ser Arg Lys Asn Thr Glu Phe Leu Arg

Gly Lys Pro Thr Ser Arg Glu Val Phe Ser Gln His Pro Tyr Ala Glu
595 600 605

Asn Phe Ile Gly Lys Pro His Val Trp Thr Val Asp Tyr Asn Asn Ser
610 615 620

Glu Glu Phe Glu Ala Ala Ile Lys Ala Ile Met Arg Thr Gln Val Asp 625 630 635 640

Pro Tyr Leu Pro Tyr Glu Tyr Thr Cys Glu Gly Met Leu Glu Arg Ile
645 650 655

Thr Ala Tyr Ile Gln His Gln Asp Phe Cys Arg Ala Ser Glu His Cys
660 665 670

His Pro Pro Ser Phe Ile Ile Arg Ser Leu Ser Arg Ala Thr Pro
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<212> PRT

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Thr Al		Ser	Thr	Thr	Ser 55	Ser	Ser	Gln	Ala	Ser 60	Pro	Pro	Pro	Glu
Arg Cy 65	s Ser	Pro	Ser	Ile 70	Pro	Thr	Arg	Arg	Thr	Ser	Ser	Ala	Ser	Pro
Thr Cy	s Gly	Gln	Ser 85	Thr	Thr	Thr	Thr	Gln 90	Arg	Ser	Leu	Lys	Gln 95	Pro
Ser Ar	g Pro	Leu 100	Glu	Leu	Arg	Thr	Pro 105	Thr	Tyr	Pro	Thr	Ser 110	Thr	Pro
Ala Ar	g Gly 115	Cys	Trp	Ser	Gly	Ser 120	Thr	Pro	Thr	Ser	Ser 125	Thr	Arg	Thr
Ser Al		Leu	Gln	Thr	Thr 135	Ala	Leu	Pro	Glu	Ala 140	His	Ala	Pro	Gln
Ser Pr	o Phe	Val	Leu	Ala 150	Pro	Asn	Ala		His 155	Leu	Glu	Trp	Ala	Arg
Asn Th	r Ser	Leu		Pro	Gly	Ala	Trp	Pro	Pro	Arg	Thr	Pro	Cys	Gly

Pro Gly Trp Pro Cys Leu Gly Gly Pro Ala Pro Thr Pro Ala Trp Thr

165

170

175

12

180 185 190

Thr Gly Ser Val Ser Pro Pro Ser Ser Pro Ser Thr Ala Arg Thr Pro

Ser Ser Ser Cys Arg Cys Pro Val Thr Ala Pro Ser Arg Arg Thr Thr
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Cys Thr Leu Gly Val Arg Pro Ala Trp Pro Gly Val Leu Pro Ala Glu
225 230 235 240

Gly Ala Ser Ala Leu Gln Cys Ala Gly Ser Asn I.. Lys Tyr Arg Arg

245 250 255

Leu Cys Pro Cys Arg Asp Phe Arg Lys Arg Asn Ser Gly Arg Asn Ser
260 265 270

Gly Ile Leu Leu Leu Phe Thr Ser Arg Val Phe Phe Leu Phe Phe Phe 275 280 285

Lys Ser Phe Val Ala Tyr Leu Lys Leu Pro Phe Phe Ser Gln Val Cys
290 295 300

Leu Phe Ala Ser Ser Glu Met Phe Phe Thr Ile Ser Arg Lys Asn Met

305 310 315 320

Ser Gln Lys Leu Ser Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly
325 330 335

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13.

Leu	Met	Leu	Leu	His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser
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Val Lys Leu Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys
355 360 365

Ala Leu Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala
370 375 380

Ser Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu 385 390 395 400

Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp Tyr
405 410 415

Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr Ser Gly
420 425 430

Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val Ser Gly Ser
435
440
445

Ile Arg Ile Ala Val Glu Asn His Leu Val Leu Leu His Pro Leu Trp
450 455 460

Ile Ile Ser Tyr Gly Arg Lys Ala Leu Tyr Cys Trp Leu Arg Thr Glu
465 470 475 480

Ala Ile Leu Tyr Asn Lys Ser Thr Asn Gly Gly Gln Asp Lys Cys Val
485 490 495

Phe	Pro	Pro	Ile	Asp	Gly	Tyr	Pro	His	Tyr	Glu	Gly	Lys	Ile	Lys	Trp
			500					505					510		

Ile Asn Asp Met Cys Arg Ser Asp Pro Cys Lys Ala His Tyr Gly Ile
515 520 525

Asp Gly Ser Ser Cys Thr Phe Phe Ile Tyr Leu Ser Asp Ala Asp Asn 530 535 540

His Cys Pro His Ala Pro Trp Arg His Lys Asn Pro Tyr Asp Asp Ala 545 550 555 560

Glu His Asn Ser Cys Ala Glu Ile Arg Ser Asp Phe Glu Leu Leu Tyr

565 575

Ser Val Ile His His Lys Asp C . Phe I. Phe Met Arg Leu Arg Arg 580 585 590

Arg Arg Met Val Glu Gly Trp Ala Gln Ile Ala Lys Ser Leu Ala Asp
595 600 605

Lys Gln Asn Ala Glu Lys Lys Lys Arg Lys Lys Ala Leu Val His Leu
610 615 620

Gly Ile Ile Thr Lys Asp Thr Val Ser Lys Ile Ala Glu Thr Gly Phe 625 630 635 640

Ser Ala Ala Pro Leu Gly Asp Leu Val His Trp Ser Asp Val Ile Thr

Ser Ala Tyr Ala Ala Gly His Asp Val Arg Ile Thr Ala Ser Leu Ala

Glu Leu Lys Asp Val Val Lys Lys Ile Ile Gly Asn Arg Ser Gly Cys

Pro Ser Val Gly Asp Arg Ile Val Glu Leu Leu Tyr Ala Asp Val Ile

Gly Leu Gly Gln Phe Lys Lys Thr Leu Gly Pro Thr Trp Ala Gln His

Arg Trp Met Val Arg Val Leu Glu Thr Phe Gly Ser Asp Pro Asp Phe

Glu His Ala Asn Tyr Ala Gln Thr Lys Gly His Lys Ser Pro Trp Gly

Trp Trp Asn Leu Asn Pro Asn Asn Phe Tyr Thr Met Phe Pro His Thr

Pro Glu Asn Thr Phe Leu Gly Phe Ala Ile Glu Gln His Leu Asn Ser

Ser Asp Met His His Leu Asn Glu Met Lys Arg Gln Asn Gln Thr Leu

Val	Tyr	Gly	Lys	Val	Asp	Ser	Phe	Trp	Lys	Asn	Lys	His	Ile	Tyr	Phe
				805					810					815	

Glu Ile Ile His Asn Tyr Ile Glu Val Gln Ala Thr Val Tyr Asp Ser
820 825 830

Ser Thr Pro Asn Ile Pro Ser Tyr Ser Arg Asn His Gly Ile Leu Ser
835 840 845

Gly Arg Asp His Arg Phe Leu Leu Arg Glu Thr Phe Leu Leu Gly
850 855 860

Leu Gly Thr Pro Tyr Glu Arg Cys Ala Pro Leu Glu Ala Met Ala Asn 865 870 875 880

Arg Cys Val Phe Leu Lys Pro Lys Phe Pro Tro Pro Asn Ser Arg Lys
885 890 895

Asn Thr Glu Phe Leu Arg Gly Lys Pro Thr Ser Arg Glu Val Phe Ser

Gln His Pro Tyr Ala Glu Asn Phe Ile Gly Lys Pro His Val Trp Thr
915 920 925

Val Asp Tyr Asn Asn Ser Glu Glu Phe Glu Ala Ala Ile Lys Ala Ile
930 935 940

Met Arg Thr Gln Val Asp Pro Tyr Leu Pro Tyr Glu Tyr Thr Cys Glu 945 950 955 960 Gly Met Leu Glu Arg Ile Thr Ala Tyr Ile Gln His Gln Asp Phe Cys 965 970 975

Arg Ala Ser Glu His Cys His Pro Pro Ser Phe Ile Ile Arg Ser Leu
980 985 990

Ser Arg Ala Thr Pro Pro Thr Ser Leu Gly Leu Leu His Leu Pro
995 1000 1005

Gly Gly Ser Pro Gly Ser Trp Glu Leu Val Glu Gly Pro Gly Trp Thr
1010 1015 1020

Leu Pro Val Gly Val Pro Ser Arg Pro Gly Arg Pro Leu Gln Pro Gln
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Asn His Asp Gly Lys Lys Ser Ile Cys Ser Gln Gly Leu Thr Phe Gly

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1050
1055

Gly Lys Ala Ile Glu Thr Leu Phe Phe Ser Leu Phe Leu Lys Ile Tyr

1060 1065 1070

Phe Phe Lys Ile Phe Tyr Leu Asp Val Arg Cys Arg Arg Glu Lys Lys
1075 1080 1085

Lys Lys Lys Lys Arg Gly Arg Lys Leu Ile Pro Phe Ser Glu Gly
1090 1095 1100

Phe Lys Lys Gln Lys Asn Ser Gly Leu Ser Ser Ala Arg Thr Val Thr

18

1110 1115 1120

Ile Tyr Ser Cys Gln Glu Leu Ser Pro His Val Trp Lys Ser Ser Ile 1125 1130 1135

Leu Glu Thr Pro Cys Glu Tyr Thr Asn Gln His Ser Leu Leu Asn Ser

1140 1145 1150

His Ser His Ile Val Leu Thr Asp Ser Gln Gly Thr Pro Arg Gly Phe
1155 1160 1165

Cys Leu Tyr Lys Ile Asn Gln Gln Met Val Lys Ser Leu Asn Lys His
1170 1175 1180

Gly Leu Lys Ala Ser Arg Leu Leu Arg Trp Arg Val Ser Pro Ser Pro 1185 1190 1195 1200

Cys Leu Ile Asn Asp Cys Ile His Asn Ser Ser Lys Val Asp Gly Lys

1205 1210 1215

Val Ser Ile Phe Gln Ile Arg Ala Tyr Tyr Gln Arg Leu Lys Asp Ile
1220 1225 1230

Pro Gly Pro Pro Ala Asn Ala Phe Trp Asn His Leu His Ile Gln Thr
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His Arg Lys Gln Gln Arg Gly Asn Thr His Ala Ser Gln Lys Pro Phe
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Ile Pro Leu Gly Lys Gly Gly Arg Glu Gly Ser Pro Thr Leu Glu Lys
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Pro Gly Leu His Arg Gln Gly Ser Tyr Cys Pro Leu Val Leu Ile Trp 1285 1290 1295

Glu Ser Lys Lys Val Tyr Leu Val Glu Thr Lys Pro Asn Ser Thr Lys

1300 1305 1310

Phe Phe Asn Tyr Cys Val Ser Ala Ala Leu Val Gly Ala Trp Lys Thr
1315 1320 1325

Ser Ser Gly Glu Asp Ile Ala Leu Glu Leu Thr Ser Cys Gly Phe Ser 1330 1335 1340

Phe Phe Phe Phe Phe Phe Phe Leu Arg Gln Ser Leu Thr Val Ser 1345 1350 1355 1360

Pro Arg Leu Glu Cys Ile Phe Leu Cys Pro Thr Lys Thr His Ile Pro
1365 1370 1375

Ser Gln Leu Thr Ala Thr Ser Thr Ser Gln Val Gln Glu Met Leu Leu
1380 1385 1390

Pro Pro Pro Lys Leu Gly Ser Gln Ala Cys Ala Thr Thr Pro Ser Val

Leu Tyr Phe Lys Arg Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser 1410 1415 1420 Asn Ser Pro Lys Val Ile His Leu Pro Trp Leu Pro Lys Met Leu Asp 1425 1430 1435 1440

Tyr Arg Cys Glu Pro Leu His Leu Ala Ser Lys Ile Ser Ile Trp Gln
1445 1450 1455

Ile His Ile Ala Thr Phe Ile Leu Val Lys Ile Pro Lys Cys Phe His
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Thr Ser Gln Lys Ala Thr Arg Asn Ser Ala Trp Thr Pro 1475 1480 1485

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<212> DNA

<213> Homo sapiens

<400> 5

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21

ggtcaagata aatgcgtttt tccaccgatc gacggttacc cacactacga gggaaaaatt 600 aagtggataa atgacatgtg ccgttcggat ccgtgcaagg ctcattatgg tatagatggg 660 tecagetgea ettetetat ataceteagt gaegeegaea ateategtee eeatgeacee 720 tggagacata aaaatcctta cgacgacgct gagcataatt catgcgctga aattcgtagt 780 gattttgaac ttctgtacag tgtgattcat cataaggacg agttccattt tatgagacta 840 cggagacggc gaatggttga gggatgggcc caaatcgcaa agtccctagc agataagcag 900 aacgcagaga agaaaaaacg gaaaaaggcc ctagttcacc tgggaatcat taccaaggac 960 actgtatcta agattgctga aacaggtttc agtgccgcac ctcttggtga cttagttcat 1020 tggagtgatg taattacate tgegtaegea geggggeatg aegttaggat caetgeatea 1080 ctggctgagc tcaaggatgt cgtgaagaag attataggta accgatctgg ttgcccatct 1140 gtaggagaca gaattgttga gctactttac gctgatgtaa ttggactcgg tcaattcaag 1200 aaaactctag gtccaacctg ggctcaacat cggtggatgg ttcgagtcct tgaáactttt 1260 ggatcagatc ccgattttga acatgccaat tatgcgcaaa caaagggtca caagagccct 1320 tggggatggt ggaatctgaa ccctaataac ttttatacaa tgttccccca tactccagaa 1380 aacacttttc ttgggtttgc gatcgagcag cacctaaact ccagtgatat gcaccacctt 1440 aatgagatga agaggcagaa tcagacgctt gtgtatggca aagtggatag cttctggaag 1500 aataagcata tttacttcga aatcattcac aattacatcg aagtgcaagc aactgtgtat 1560 gacteeteta cacceatat tecetettae tetegaaace aeggtattet ttetggtegg 1620 gaccatcgat tectectecg agagaeette ttgttactag gactagggae teettacgaa 1680 egttgegete egetggaage catggeaaat egatgegtet tteteaaace gaagtteece 1740 ccacccatt caaggaagaa tacagagttt ttacgaggca agcccacctc cagagaggtg 1800 ttctcccagc atccctacgc ggagaacttc atcggcaagc cccacgtgtg gacagtcgac 1860 tacaacaact cagaggagtt tgaagcagcc atcaaggcca ttatgagaac tcaggtagac 1920 ccctacctac cctacgagta cacctgcgag gggatgctgg agcggatcac cgcctacatc 1980 cagcaccagg acttetgeag agetteagaa caetgecaee caeccagttt tataateege 2040 teceteteca gggcaacece acceaceage etaggeetge tectecacet teegggagge 2100 agccccggga getgggaget ggtggagggg ccaggetgga cgettecegt gggagtecec 2160 tccagacctg gtcggcccct gcagccacag aaccacgatg gcaaaaaatc tatttgttct 2220 caaggactaa cetttggggg gaaagcaata gagacactet ttttctetet ttttttaaaag 2280

22.

atttatttct ttaaataa 2298

<210> 6

<211> 765

<212> PRT

<213> Homo sapiens

<400> 6

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser Leu

5 10 15

Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu His Tyr

20 25 30

Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu Arg Glu Gln

35 40 45

Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu Ala Glu Glu Asn

50 55 60

Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser Met Ala Gly Tyr Ala 65 · 70

Asp Leu Lys Arg Thr Ile Ala Val Leu Leu Asp Asp Ile Leu Gln Arg

85 90 95

75

80

Leu Val Lys Leu Glu Asn Lys Val Asp Tyr Ile Val Val Asn Gly Ser

100 105 110

Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr	Ser	Gly	Asn	Leu	Val	Pro	Val	Thr
		115					120					125			

Thr Asn Lys Arg Thr Asn Val Ser Gly Ser Ile Arg Ile Ala Val Glu
130 135 140

Asn His Leu Val Leu Leu His Pro Leu Trp Ile Ile Ser Tyr Gly Arg

Lys Ala Leu Tyr Cys Trp Leu Arg Thr Glu Ala Ile Leu Tyr Asn Lys

165 170 175

Ser Thr Asn Gly Gly Gln Asp Lys Cys Val Phe Pro Pro Ile Asp Gly
180 185 190

Tyr Pro His Tyr Glu Gly Lys Ile Lys Trp Ile Asn Asp Met Cys Arg

195 200 205

Ser Asp Pro Cys Lys Ala His Tyr Gly Ile Asp Gly Ser Ser Cys Thr
210 215 220

Phe Phe Ile Tyr Leu Ser Asp Ala Asp Asn His Cys Pro His Ala Pro 225 230 235 240

Trp Arg His Lys Asn Pro Tyr Asp Asp Ala Glu His Asn Ser Cys Ala
245 250 255

Glu Ile Arg Ser Asp Phe Glu Leu Leu Tyr Ser Val Ile His His Lys
260 265 270

Asp	Glu	Phe	His	Phe	Met	Arg	Leu	Arg	Arg	Arg	Arg	Met	Val	Glu	Gly
		275					280					285			

Trp Ala Gln Ile Ala Lys Ser Leu Ala Asp Lys Gln Asn Ala Glu Lys
290 295 300

Lys Lys Arg Lys Lys Ala Leu Val His Leu Gly Ile Ile Thr Lys Asp
305 310 315 320

Thr Val Ser Lys Ile Ala Glu Thr Gly Phe Ser Ala Ala Pro Leu Gly
325 330 335

Asp Leu Val His Trp Ser Asp '37 The Ser Ala Tyr Ala Ala Gly
340

His Asp Val Arg Ile Thr Ala Ser Leu Ala Glu Leu Lys Asp Val Val

Lys Lys Ile Ile Gly Asn Arg Ser Gly Cys Pro Ser Val Gly Asp Arg 370 375 380

Ile Val Glu Leu Leu Tyr Ala Asp Val Ile Gly Leu Gly Gln Phe Lys
385 390 395 400

Lys Thr Leu Gly Pro Thr Trp Ala Gln His Arg Trp Met Val Arg Val
405 410 415

Leu Glu Thr Phe Gly Ser Asp Pro Asp Phe Glu His Ala Asn Tyr Ala

25

420 425 430

Gln Thr Lys Gly His Lys Ser Pro Trp Gly Trp Trp Asn Leu Asn Pro
435
440
445

Asn Asn Phe Tyr Thr Met Phe Pro His Thr Pro Glu Asn Thr Phe Leu
450 455 460

Gly Phe Ala Ile Glu Gln His Leu Asn Ser Ser Asp Met His His Leu
465 470 475 480

Asn Glu Met Lys Arg Gln Asn Gln Thr Leu Val Tyr Gly Lys Val Asp
485
490
495

Ser Phe Trp Lys Asn Lys His Ile Tyr Phe Glu Ile Ile His Asn Tyr
500 505 510

Ile Glu Val Gln Ala Thr Val Tyr Asp Ser Ser Thr Pro Asn Ile Pro
515 520 525

Ser Tyr Ser Arg Asn His Gly Ile Leu Ser Gly Arg Asp His Arg Phe
530 535 540

Leu Leu Arg Glu Thr Phe Leu Leu Gly Leu Gly Thr Pro Tyr Glu
545 550 555 560

Arg Cys Ala Pro Leu Glu Ala Met Ala Asn Arg Cys Val Phe Leu Lys
565 570 575

705

Pro	Lys	Phe	Pro	Pro	Pro	Asn	Ser	Arg	Lys	Asn	Thr	Glu	Phe	Leu	Arg
			580					585					590		
				•											
Gly	Lys	Pro	Thr	Ser	Arg	Glu	Val	Phe	Ser	Gln	His	Pro	Tyr	Ala	Glu
		595					600					605			
Asn			Gly	Lys	Pro		Val	Trp	Thr	Val	Asp	Tyr	Asn	Asn	Ser
	610					615					620				
		_,													
	Glu	Phe	Glu	Ala	Ala	Ile	Lys	Ala	Ile		Arg	Thr	Gln	Val	
625					630					635					640
Pro	Tvr	Leu	Pro	Tvr	Glu	Tvr	Thr	Cvs	Glu	Glv	Met	T.e.ii	Glu	A.r.a	Tla
	-,-			645		-1-		•,,.	650	Cly		DCU	GIU	655	116
Thr	Ala	Tyr	Ile	Gln	His	Gln	Asp	Phe	Cys	Arg	Ala	Ser	Glu	His	Cys
			660					665					670		
His	Pro	Pro	Ser	Phe	Ile	Ile	Arg	Ser	Leu	Ser	Arg	Ala	Thr	Pro	Pro
		675					680					685			
Thr	Ser	Leu	Gly	Leu	Leu	Leu	His	Leu	Pro	Gly	Gly	Ser	Pro	Gly	Ser
	690					695					700				
Trp	Glu	Leu	Val	Glu	Gly	Pro	Gly	Trp	Thr	Leu	Pro	Val	Glv	Val	Pro

Ser Arg Pro Gly Arg Pro Leu Gln Pro Gln Asn His Asp Gly Lys Lys
725 730 735

715

720

710

Ser Ile Cys Ser Gln Gly Leu Thr Phe Gly Gly Lys Ala Ile Glu Thr
740 745 750

Leu Phe Phe Ser Leu Phe Leu Lys Ile Tyr Phe Phe Lys
755 760 765

<210> 7

<211> 948

<212> DNA

<213> Homo sapiens

<400> 7

cggetettac egeageetga gttteageag etgetgegea aggecaaact etteeteggg 60
tttggettee eetacgaggg eecegeece etggaggeea tegecaatgg ttgeatette 120
etgeagteee getteageee geeceacage teeeteace aegagttett eecaggeaag 180
eccaceteea gagaggtgtt eteeeageat eectacgegg agaactteat eggeaageee 240
caegtgtgga eagtegaeta eaacaactea gaggagtttg aageageeat caaggeeatt 300
atgagaacte aggtagaeee etacetaeee taegagtaea eetgegaggg gatgetggag 360
eggateeaeg eetacateea geaceaggae tteetgeagag eteeagaeea etgeeetaee 420
agaggeeeae geeeegeaga geeeetttgt eetggeeeee aatgeeaee aectggagtg 480
etggeeggae etgggagge etgeacegae aectgeetgg aecaeeet gegggeetgg 540
etggeegtge etgggaggge etgeacegae aectgeetgg aecaegget aatetgtgag 600
eeeteettet teeeetteet gaacageeag gaegeettee teaagetgea ggtgeeetgg 720
agtgetaeet geagaaggag eetetegete teagtgege ggeteeaaea eeagtaeeg 780
eeggetetge eeetgeegg aetteegeaa geggaattee ggeeggaatt eeggaattet 840
tttgettttt aegagtegag tttttttet tttttttte aagtettgat ttgtggetta 900

28.

cctcaagtta ccatttttca gtcaagtctg tttgtttgct tcttcaga

948

<210> 8

<211> 1295

<212> DNA

<213> Homo sapiens

<400> 8

ggccgcaagc ttattccctt tagtgagggt taatttaaaa agcaaaagaa ttccggcctg 120 ageteageta ggaeagtgae tatttaatat agttaatgee aggaaettte accceaegta 180 tggaagagtt caatcttaga gtagacacct tgtgaataca caaaccaaca ctcccttctg 240 aatteteatt eetageacat tgteettaca gatteecagg ggacaccaag aggtttttge 300 ctatataaaa ttaactagca acagtaaatg gtgaagtcct aattaaataa gcatgggtta 360 aaagccagtc gtctgctaag atggtgaagg gtgtccccat ccccatgttt aataaatgat 420 tgctgaatcc acaattcctc taaagttgat gggaaagttt ccatctttca gataagagca 480 tattatcaac ggttaaagga tatcccaggc cctccagcaa atgccttctg gaatcatctc 540 cacattcaga cacatcgtaa acaacagagg ggcaatactc atgcttcgca aaagccgttc 600 attccccttg gcaaaggcgg gagagaggc tcaccaacct tggagaagcc tggtttacat 660 cgtcaaggta gctactgccc tctagtgttg atatgggaat aaagcaaaaa agtatacctg 720 gttgaaacga aaccgaactc cacaaagttt ttcaattact gatgtgtctc agcagccttg 780 gtaggagett ggaaaacate ateaggtgag gatattgeae tggagetgae etettgtgge 840 ttctaaagtt tcttttttt tttttttt tttttgagac agagtctcac tgtgtcaccc 900 aggctggagt gcattttctt gtgtccaacc aagactcaca taccatctca gctcactgca 960 acctccacct cccaggttca agagatgete etgecetage eteccaagta getgggatca 1020 caggcatgtg ccaccacac cagctaagtt ttgtattttt agaagagatg gggtttcacg 1080 atgttggcca gactggtctc gaactcctga cctaaagtga tccacctgcc ttggcttccc 1140 aaaatgctgg attacaggtg tgaaccactg cacctggcct ccaagatttc tatttggcaa 1200 attcacatag ctactttcat acttgttaaa ataccgaaat gcttccatac cagttagcaa 1260

aaggccaccc ggaattcagc ttggacttaa ccagg

1295

<210> 9

<211> 2298

<212> DNA

<213> Homo sapiens

<400> 9

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ggatcagatc ccgattttga acatgccaat tatgcgcaaa caaagggtca caagagccct 1320 tggggatggt ggaatctgaa ccctaataac ttttatacaa tgttccccca tactccagaa 1380 aacacttttc ttgggtttgc gatcgagcag cacctaaact ccagtgatat gcaccacctt 1440 aatgagatga agaggcagaa tcagacgctt gtgtatggca aagtggatag cttctggaag 1500 aataagcata tttacttcga aatcattcac aattacatcg aagtgcaagc aactgtgtat 1560 gacteeteta cacceaatat teeetettae tetegaaace aeggtattet ttetggtegg 1620 gaccategat tectecteeg agagacette ttgttactag gactagggae teettacgaa 1680 cgttgcgctc cgctggaagc catggcaaat.cgatgcgtct ttctcaaacc gaagttcccc 1740 ccacccaatt caaggaagaa tacagagttt ttacgaggca agcccacctc cagagaggtg 1800 ttctcccagc atccctacgc ggagaacttc atcggcaagc cccacgtgtg gacagtcgac 1860 tacaacaact cagaggagtt tgaagcagcc atcaaggcca ttatgagaac tcaggtagac 1920 ccctacctac cctacgagta cacctgcgag gggatgctgg agcggatcac cgcctacatc 1980 cagcaccagg acttctgcag agcttcagaa cactgccacc cacccagttt tataatccgc 2040 teceteteca gggcaacece acettecea teceagggta aceegactae acggetaaga 2100 cttgttctac cgccgtttcc agaactagcc gggccttgta gtcaccggaa ccacccggg 2160 ggtaaaaaat tatattggtt ttctcgtact aatttatggg gtgaatctaa tcgtgatact 2220 ttatttttat cttttttaa agatttattt ttagaaatta ttaaatattt ttattgggat 2280 gttcgttgtc gtcgttaa 2298

<210> 10

<211> 765

<212> PRT

<213> Homo sapiens

<400> 10

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser Leu

1 5 10 15

Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu His Tyr

31.

20 25 30

Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu Arg Glu Gln
35 40 45

Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu Ala Glu Glu Asn
50 55 60

Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser Met Ala Gly Tyr Ala
65 70 75 80

Asp Leu Lys Arg Thr Ile Ala Val Leu Leu Asp Asp Ile Leu Gln Arg

85 90 95

Leu Val Lys Leu Glu Asn Lys Val Asp Tyr Ile Val Val Asn Gly Ser

Ala Ala Asn Thr Thr Asn Gly Thr Ser Gly Asn Leu Val Pro Val Thr

Thr Asn Lys Arg Thr Asn Val Ser Gly Ser Ile Arg Ile Ala Val Glu
130 - 135 140

Asn His Leu Val Leu Leu His Pro Leu Trp Ile Ile Ser Tyr Gly Arg

145 150 155 160

Lys Ala Leu Tyr Cys Trp Leu Arg Thr Glu Ala Ile Leu Tyr Asn Lys

165 170 175

.

Ser	Thr	Asn-	Gly	Gly	Gln	Asp	Lys	Cys	Val	Phe	Pro	Pro	Ile	Asp	Gly
			180					185					190		
Tyr	Pro	His	Tyr	Glu	Gly	Lys	Ile	Lys	Trp	Ile	Asn	Asp	Met	Cys	Arg
		195					200					205			
Ser	Asp	Pro	Cys	Lys	Ala	His	Tyr	Gly	Ile	Asp	Gly	Ser	Ser	Cys	Thr
	210					215					220				
Phe	Phe	Ile	Tyr	Leu	Ser	Asp	Ala	Asp	Asn	His	Cys	Pro	His	Ala	Pro
225					230					235					240
Trp	Arg	His	Lys	Asn	Pro	Tyr	Asp	Asp	Ala	Glu	His	Asn	Ser	Cys	Ala
				245					250					255	
Glu	Ile	Arg	Ser	Asp	Phe	Glu	Leu	Leu	Tyr	Ser	Val	Ile	His	His	Lys
			260					265					270		
Asp	Glu	Phe	His	Phe	Met	Arg	Leu	Arg	Arg	Arg	Arg	Met	Val	Glu	Gly
		275					280					285			
Trp	Ala	 Gln	Ile	Ala	Lys	Ser	Leu	Ala	Asp	Lys	Gln	Asn	Ala	Glu	Lys
	290					295					300				
Lys	Lys	Arg	Lys	Lys	Ala	Leu	Val	His	Leu	Gly	Ile	Ile	Thr	Lys	Asp
305					310					315		•			320
Thr	Val	Ser	Lys	Ile	Ala	Glu	Thr	Gly	Phe	Ser	Ala	Ala	Pro	Leu	Gly

Asp	Leu	Val	His	Trp	Ser	Asp	Val	Ile	Thr	Ser	Ala	Tyr	Ala	Ala	Gly
			340					345					350		

His Asp Val Arg Ile Thr Ala Ser Leu Ala Glu Leu Lys Asp Val Val
355 360 365

Lys Lys Ile Ile Gly Asn Arg Ser Gly Cys Pro Ser Val Gly Asp Arg 370 375 380

Ile Val Glu Leu Leu Tyr Ala Asp Val Ile Gly Leu Gly Gln Phe Lys
385 390 395 400

Lys Thr Leu Gly Pro Thr Trp Ala Gln His Arg Trp Met Val Arg Val
405 410 415

Leu Glu Thr Phe Gly Ser Asp Pro Asp Phe Glu His Ala Asn Tyr Ala
420 425 430

Gln Thr Lys Gly His Lys Ser Pro Trp Gly Trp Trp Asn Leu Asn Pro
435 440 445

Asn Asn Phe Tyr Thr Met Phe Pro His Thr Pro Glu Asn Thr Phe Leu
450 455 460

Gly Phe Ala Ile Glu Gln His Leu Asn Ser Ser Asp Met His His Leu
465 470 475 480

Asn Glu Met Lys Arg Gln Asn Gln Thr Leu Val Tyr Gly Lys Val Asp

34/

485 490 495

Ser Phe Trp Lys Asn Lys His Ile Tyr Phe Glu Ile Ile His Asn Tyr
500 505 510

Ile Glu Val Gln Ala Thr Val Tyr Asp Ser Ser Thr Pro Asn Ile Pro
515 520 525

Ser Tyr Ser Arg Asn His Gly Ile Leu Ser Gly Arg Asp His Arg Phe
530 535 540

Leu Leu Arg Glu Thr Phe Leu Leu Gly Leu Gly Thr Pro Tyr Glu
545 550 555 560

Arg Cys Ala Pro Leu Glu Ala Met Ala Asn Arg Cys Val Phe Leu Lys

565 570 575

Pro Lys Phe Pro Pro Pro Asn Ser Arg Lys Asn Thr Glu Phe Leu Arg
580 585 590

Gly Lys Pro Thr Ser Arg Glu Val Phe Ser Gln His Pro Tyr Ala Glu
595 600 605

Asn Phe Ile Gly Lys Pro His Val Trp Thr Val Asp Tyr Asn Asn Ser
610 615 620

Glu Glu Phe Glu Ala Ala Ile Lys Ala Ile Met Arg Thr Gln Val Asp
625 630 635 640

660

WO 00/08171 PCT/CA99/00711

Pro Tyr Leu Pro Tyr Glu Tyr Thr Cys Glu Gly Met Leu Glu Arg Ile

645 650 655

670

35.

Thr Ala Tyr Ile Gln His Gln Asp Phe Cys Arg Ala Ser Glu His Cys

665

His Pro Pro Ser Phe Ile Ile Arg Ser Leu Ser Arg Ala Thr Pro Pro

675 680 685

Phe Pro Phe Gln Gly Asn Pro Thr Thr Arg Leu Arg Leu Val Leu Pro
690 695 700

Pro Phe Pro Glu Leu Ala Gly Pro Cys Ser His Arg Asn His Pro Gly
705 710 715 720

Gly Lys Lys Leu Tyr Trp Phe Ser Arg Thr Asn Leu Trp Gly Glu Ser
725 730 735

Asn Arg Asp Thr Leu Phe Leu Ser Phe Phe Lys Asp Leu Phe Leu Glu
740 745 750

Ile Ile Lys Tyr Phe Tyr Trp Asp Val Arg Cys Arg Arg
755 760 765

<210> 11

<211> 237

<212> DNA

<213> Homo sapiens

<400> 11

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<210> 12

<211> 78

<212> PRT

<213> Homo sapiens

<400> 12

Pro Phe Pro Phe Gln Gly Asn Pro Thr Thr Arg Leu Arg Leu Val Leu

1 5 10 15

Pro Pro Phe Pro Glu Leu Ala Gly Pro Cys Ser His Arg Asn His Pro
20 25 30

Gly Gly Lys Lys Leu Tyr Trp Phe Ser Arg Thr Asn Leu Trp Gly Glu

35 40 45

Ser Asn Arg Asp Thr Leu Phe Leu Ser Phe Phe Lys Asp Leu Phe Leu
50 55 60

Glu Ile Ile Lys Tyr Phe Tyr Trp Asp Val Arg Cys Arg Arg
65 . 70 . 75

37

<210>	13
<211>	28
<212> 1	DNA
<213>	Artificial Sequence
<220>	
<223> 1	Description of Artificial Sequence:primer
<400>	13
cagacci	tggt eggeecetge agecaeag 2
<210>	14
<211> 2	24
<212> I	ONA
<213> 1	Artificial Sequence
<220>	
<223> I	Description of Artificial Sequence:primer
<400> 1	
ggaggca	agec eegggagetg ggag 24
	_
<210> 1 <211> 3	
<211> 3	
	artificial Sequence
~&&J/ }	retreat seducuee
<220>	•
	Description of Artificial Sequence:primer

38,

400> 15	
gtcaagata aatgegtttt tecaeegate	30
210> 16	
211> 34	
212> DNA	
213> Artificial Sequence	
220>	
223> Description of Artificial Sequence:primer	٠
100> 16	

34

gtggattata tcctatggca gaaaagcttt atat